

105090" 92988460

45

Hum_PTP1B	1	DFPCRVAKLPKNKN	20	RNRYRDVSPFDHSHRIKLHQE	30	40	50	60	DN
Hum_TCPTP		DYHRVAKFPENRN		RNRYRDVSPYDHSRV IQNA					EN
Hum_PTP_xi_D1		GITADSSNHPDNKH		KNRYINIVAYDHSRVKLAQL					AEK
Hum_PTP_zeia_D1		GITADSSNHPDNKH		KNRYINIVAYDHSRVKLAQL					AEK
Hum_PTP_gamma_D		NITAEHSNHPDNKH		KNRYINILAYDHSRVKLRPL					PGK
Dros_PTP99A_D1		DLPCHEHSQHPENKR		KNRYINILAYDHSRVVHLHPT					PGQ
Hum_LCA_D1		QFTWENSNLVKNP		KNRYANVIAVDHSRVILTSI					DGV
Hum_PTP_mu_D1		SAPWDSAKKDENRM		KNRYGNIIAYDHSRVRLQTI					EGD
Hum_PTP_alpha_D1		QATCEAASKEENKE		KNRYVNILPYDHSRVHLTPV					EGV
Hum_PTP_opsilon_D		QGTFFELANKENRE		KNRYPNILPNDHSRVILSQL					DGI
Mouso_CD45_D1		KFPIKDARKPHNQN		KNRYVDILPYDYNRVELSEI					NGD
Hum_SH_PTP2		LYSRKEGQRQENKN		KNRYKNILPFDHTRVVLHDG					DPN
Hum_SH_PTP1		LHQLEGGQRPENKG		KNRYKNILPFDHSHRVILQGR					DSN
Hum_PTP_boia		NQSCDIALLPENRG		KNRYNNILPYDATRVKLSNV					DDD
Dros_PTP10D		DQPCTFADLPCNRP		KNRYTNILPYDHSRFLQPV					HEE
Hum_SAP.1		SQSOMVASASENNA		KNRYRNVLPHYDWSRVPLKPI					DPE
Ral_PTP_STEP		FVDPKEYDIPGLVR		KNRYKTILPNPHSRVRLTSP					NGL
Dros_PTP69A_D1		DRTTKNSDLKENAC		KNRYPDIKAYDQTRVKLAVI					SGH
Hum_MEG2		VGTFHCSMSPGNLE		KNRYGDPVCLDQTRVKLTKR					TPS
Hum_PTP_PEST		IYPTATGEKEENVK		KNRYKDILPFDHSHRVKLTJK					EDY
Hum_PTPH1		GLAITFAKLQNLD		KNRYKDVLPYDTTRVLLQGN					QDK
Dici_PTP1		PSETSEGDKKHNTS		KNRYTNILPVNHTRVQLKKI					SPS
Fiss_yeast_pyp1		QWSTVDSLSNTSYK		KNRYTDIVPYNCTRVHLKRT					KGC
Fiss_yeast_pyp2		WCCLASSRSTSISS		KNRYTDIVPYDKTRVRLAVP					AEK
Hum_PTP_xi_D2		GITADSSNHPDNKH		KNRYINIVAYDHSRVKLAQL					RGV
Hum_LCA_D2		TSRFISANLPCNKF		KNRLVNIMPYELTRVCLQPI					RGE
Hum_PTP_alpha_D2		NDKMRGTGNLPANMK		KNRVLOIIPYEFNRVILPVK					RGQ
Hum_PTP_opsilon_D2		KENMRGTGNLPANMK		KARVIOIIPYDFNRVILSMK					DGE
Mouse_CD45_D2		VEDCSIALLPNHE		KNRCMDILPPDRCLPFLITI					DDSD
Dros_PTP69A_D2		WRTQHIGNQEEENKK		KNRSNVVPYDFNRVPLKHELEMSKESEPESESSDDSD					PMR
Hum_PTP_zeia_D2		SKSCSVGENEENNM		KNRSQEIIPYDRNRVILTPL					SGE
Hum_PTP_gamma_D2		QSDYSAALKQCENRE		KNRTSSIIIPVERSRVGISSL					PGM
Hum_PTP99A_D2		VECFSAQKECNKE		KNRNSVVPSEARAVGLAPL					
Dros_PTP99A_D2		ETNLMAEOVEELKNCTPYLEQQYKNIIQFOPKDIHIASAMKOVNSIKNRGAIFPIEGSRVHLTPKP							
Yarsinia_PTP		TNDPRYLOACGGEKI		LNRFRDIOCCROTAVRAD					
PTP1Bseq.no.		30	40	50	60				

Fig. 1A

PTP1B66

Fig. 1B

99BTJL3

FIG. 1C

Hum_PTP1B	140	EKGLKCA	QYWPQKEEKEM	150	IFEDTNLKLTLISEDIKSYTVLELE	160	170	180	190	200
Hum_TCPTP		EKESVKA	QYWP TDQEM		LFKETGFSVKLLSESVKSYTVLQLE					NLTQTETREI
Hum_PTP_xi_D1		EKGRRKCD	QYWP ADGSE		EYGN FLVTQKSVQVLAAYTVTLRNTKIKKG					NINSGEETRTI
Hum_PTP_zeia_D1		EKGRRKCD	QYWP ADGSE		EYGN FLVTQKSVQVLAAYTVTLRNTKIKKG					SQKGRPSGRV
Hum_PTP_gamma_D		EKGRRKCD	QYWP TENSE		EYGN IIVTLKSTKIACVTVFSIRNTKVKKGQKGNPKGRQNERVV					SQKGRPSGRV
Dros_PTP99A_D1		ERGRKCD	MYWP KDGEV		TYGV IQVLLDEEVMSTYTVLQIKHLKLLK					KKQCNTKELV
Hum_LCA_D1		EKSRVKCD	QYWP ARGTE		TCGL IQVLLDTEVLAAYTVFALH					KSGSSEKREL
Hum_PTP_mu_D1		EVGRVKCC	KYWP DDTE		IYKD IKVTLIETELAEYVIFAVE					KRGVHEIREI
Hum_PTP_alpha_D1		ERKECKCA	QYWP DQGCW		TYGN IRVSVEDTVLVDTYVFCIQQVQ					DMTNRKQPRLI
Hum_PTP_opsilon_D		ERKECKCH	QYWP DQGCW		TYGN IRVSVEDTVLVDTYVFCIQQVQ					PDGCKAPRLV
Mouso_CD45_D1		EGNRNKCA	EYWPMEGTR		AFKD IIVTINDHKRCPDYIILNVAH					KKEKATGREV
Hum_SH.PTP2		ERGRKCD	KYWP EYALK		EYGV MRVRNVKESAADHYTLLKLSK					VQGNTERTV
Hum_SH.PTP1		EKGRNKCV	PYWP VGMQR		AYGP YSVTNCGEHDTTEYKLLQVSP					LDNGDLIREI
Hum_PTP_bola		EKGRVKCD	HYWPA DQDSL		YYGD LILQMLSESVLPETWTFIKICG					EEQLDAHRLI
Dros_PTP10D		EKGRKCD	QYWP DTPV		FYGD IKVQILNDSHYADWVFMFLC					RGSEQRIL
Hum_SAP.1		EAGRVKCE	HYWPL DSQPC		THGH LRVTLVGEEVMENWTVLLLL					QVEEQKTLV
Ral_PTP_STEP		EMN EKCT	EYWP EEQV		VHDG VEITVQKVIHTEDYRLISLR					RGTEERGL
Dros_PTP69A_D1		EYNKAKCA	KYWPKEVFDTK		QFGD ILVKFAQERKTGDYIELNVSKNKN					VGEEEDRRQI
Hum_MEG2		EGRRKCC	QYWPLEKDSRI		RFGP LTVTNLGVENMNHKKLEIH					NTEERQKRQV
Hum_PTP.PEST		EMGRKKCE	RYWPLYGEDPI		TFAP FKISCEDEQARTDYFILLLE					FQNESRRL
Hum_PTPH1		ERGRKCH	QYWP PPDVM		NHGG FHIQCSQSEDCTIAYVSMVLT					NTQTGEHTV
Dici_PTP1		ENCRKCD	RYWPEQIGGEQF		SYGNGNEVFGTYSVELVEVIQCREIITRNIR					LTFEGETRDI
Fiss_yeast_pyp1		EAGREMCT	AYWPSNGIGDK		QYGDYCVKQISEENVDSRFLFEIQ					NANFSPVKKV
Fiss_yeast_pyp2		EAGSEKCS	QYWPDKHALCLEGG		LRISVOKYETFEFLKVLHRL					DKPNGPPKYI
Hum_PTP_xi_D2		EKGRKCD	QYWP ADGSE		EYGN FLVTQKSVQVLAAYTVTLRNTKIKKG					SQKGRPSGRV
Hum_LCA_D2		EMGREKCH	QYWP AERSA		RYQY FVVDPMAEYNMPQYILFKVT					DARDGQSRTI
Hum_PTP_alpha_D2		ERGQEKCA	QYWP SDGLV		SYGD ITVELKKEECESYTVLLVT					NTRENKSRQI
Hum_PTP_opsilon_D2		EREQDKCY	QYWP TEGSV		THGE ITIEIKNDTLSEAIISIFLVTNLQPO					ARQEEQVRV
Hum_PTP_mu_D2		PA QLCP	QYWP ENGVS		RHGP IQVEFVSADLEEDIISFRINA					ARPQDGYRMV
Mouse_CD45_D2		NGDQEVCA	QYW GEGKQ		TYGD MEVEMKDTNRASAYTLFELR					HSKRKEPTV
Dros_PTP69A_D2		D GPRKCP	RYWA DDEVQ		YDH ILVKYVHSESCPYTFFVVT					NCKIDDTLKV
Hum_PTP_zeia_D2		NMAEDEFV	YWPNKDEPINCES		FKVTLMAEEHKCLSNEEKLIIFILE					ATQDDYVLEV
Hum_PTP_gamma_D2		SLAEDEFV	YWPSEESMNCFA		TVTLISKDRCLCSNEEQIIFILE					ATQDDYVLEV
Dros_PTP99A_D2		D INFA	QFWPEATPIESDH		RVKELNKTNSDYVSFVIO					SIQDDYELTV
Yarsinia_PTP		ELANORFGMPDYFR	QSGT YGSITVESKMTQOVGLGGINMYTLTI							REAGOKTISV
PTP1Bseq.no.		120	130	140	150	160				

PTP1B66

Fig. 1C

β5

β6

β7

β8

FIG. 1D

	210	220	230	240	250	260	270
Hum_PTP1B	LHFHYTTWPDF	G VPESPAFLN	FLFKVRES	GSLSP	PEHG	PVVVHCSA	IGRS GTFC
Hum_TCPTP	SHFHYTTWPDF	G VPESPAFLN	FLFKVRES	GSLNP	PDHG	PAVIHCSA	IGRS GTFS
Hum_PTP_xi_D1	TOYHYTTQWPDF	G VPEYSLPVL	TFRKAAYA	KRH	AVG	PVVVHCSA	IGRS GTFYI
Hum_PTP_zeta_D1	TOYHYTTQWPDF	G VPEYSLPVL	TFRKAAYA	KRH	AVG	PVVVHCSA	IGRS GTFYI
Hum_PTP_gamma_D1	IQYHYTTQWPDF	G VPEYALPVL	TFRSSAA	RMP	ETG	PVLVHCSA	IGRS GTFYI
Dros_PTP99A_D1	QYHYTNWPDF	G TPDHPLPVL	NFKSSAA	NPA	EAG	PIVVHCSA	IGRS GTFYI
Hum_LCA_D1	RQFQFMAWPDF	G VPEYTPILA	FLRRVKAC	NPL	DAG	PMVVHCSA	IGRS GTCFI
Hum_PTP_mu_D1	RQFHFMTGPDF	G VPHYATGLL	GFVRQVSK	SPP	SAG	PLVVHCSA	IGRS GTCFI
Hum_PTP_alpha_D1	TQFHFMTGPDF	G VPFTPIGML	KFLKVKAC	NPQ	YAG	AIVVHCSA	IGRS GTFV
Hum_PTP_opsilon_D1	SQLHFTSWPDF	G VPFTPIGML	KFLKVKCTL	NPV	HAG	PIVVHCSA	IGRS GTFI
Mouso_CD45_D1	THIQFTSWPDF	G VPEDPHLL	KLRRRVNAF	SNF	FSG	PIVVHCSA	IGRS GTFYI
Hum_SH_PTP1	WQYHFTWPDF	G VPSPDGGVL	DLFEEVHHK	QESIM	DAG	PIVVHCSA	IGRS GTFI
Hum_SH_PTP2	WHYQYLSWPDF	G VPSEPGVLS	FLDQINQR	QESLPH	AG	PIIVHCSA	IGRS GTFI
Hum_PTP_bola	RHFHYTVWPDF	G VPETQSLIQ	FLVTRDY	INRSP	GAG	PTVVHCSA	IGRS GTFI
Dros_PTP10D	RHFHTTWPDF	G VPNNPQTL	VRFRAPDR	ICA	EQR	PIVVHCSA	IGRS GTFI
Hum_SAP.1	RQFHYQAWPDF	G VPSSPDTLL	AFWRMLRQW	LDQTM	EGG	PPIVHCSA	IGRS GTGLI
Ral_PTP_STEP	KHYWFTSWPDF	K TPDRAPLL	HLVREVEEAA	QQEGPH	CS	PIIVHCSA	IGRS GTCFI
Dros_PTP69A_D1	TQYHYLTWKDF	M APEHPHGI	KFIQINSVSLQ	RG		PILVHCSA	IGRS GTGLV
Hum_MEG2	THFQFLSWPDF	G VPSSAASL	IDFLRVVRNQ	SLAVSNMG	ARSKGQC	PEPPIVVHCSA	IGRS GTFC
Hum_PTP.PEST	YQFHYVNWPDF	D VPSSFDSIL	DMISLMRKYQ	EH	DV	PICIHCSA	IGRS GTGAIC
Hum_PTPH1	THLQYVWPDF	G IPDDSSDF	LEFVYVYSLR	VDSE		PVLVHCSA	IGRS GTGLV
Dici_PTP1	TQYQYEGWPDF	N IPDHTQPF	RQLLHSITNR	QNQIIP	SSD	RNVPIIVHCSA	IGRS GTFC
Fiss_yeast_pyp1	HHYQYPNWSDC	N SPENVKSM	VEFLKYVNNSH	GSG		NTIVHCSA	IGRS GTCFI
Fiss_yeast_pyp2	HHFWVHTWDF	K THPDIESI	TGLIRCIDK	VPNDG		PMFVHCSA	IGRS GTGFI
Hum_PTP_xi_D2	TQYHYTQWPDF	G VPEYSLPVL	TFRKAAYA	KRH	AVG	PVVVHCSA	IGRS GTFYI
Hum_LCA_D2	RQFQFTDWPEQ	G VPKTGEFID	FIGQVHKT	KEQFG	QDG	PITVHCSA	IGRS GTVFI
Hum_PTP_alpha_D2	RQFHFGWPEV	G IPSDGMIS	IIAAVQKQ	QQQ	SGNH	PITVHCSA	IGRS GTGFC
Hum_PTP_opsilon_D2	RQFHFGWPEI	G IPAEGKMI	DLIAAVQKQ	QQQ	TGNH	PITVHCSA	IGRS GTGFI
Hum_PTP_mu_D2	QQFQFLGWPMYRD	TPVSKRSFL	KLIRQVDK	WQEEYNG	GEG	PTVVHCLNG	IGRS GTGFC
Mouse_CD45_D2	YQYQCTTWKGE	E LPAEPKDL	VSMIQDLK	QKLPKAS	PEGMKYH	KHASILVHCRD	IGRS GTGLFC
Dros_PTP69A_D2	TQFQYNGWPTVD	GEVPEVCR	GIIELVDQ	AYNHYNK	NNKNSGC	RSPLTVHCSL	IGRS GTSSIFV
Hum_PTP_zeta_D2	RHFQCPKWPN	PDSPISKTF	FELISVIKEE	AANR	DG	PMIVHDEHG	IGRS GTAGTFC
Hum_PTP_gamma_D2	RHFQCPKWPN	PDAPISSTF	FELINVIKEE	ALTR	DG	PTIVHDEYGA	IGRS VASAGMLC
Dros_PTP99A_D2	KMLHCPSPWEM	SNENSIYDF	IVDVHERCNDY	RNG		PIVIVDRIY	IGRS GGAOACTFC
Yarsinia_PTP	PVVHVGNWPD	OTAVSSEV	TKALASLV	DOTAETKRN	MYESKGS	SAVADDSKLR	PIVHCRAGVGR
PTP1Bseq.no.	180	190	200	210	220		

PTP1B66

Fig. 1D

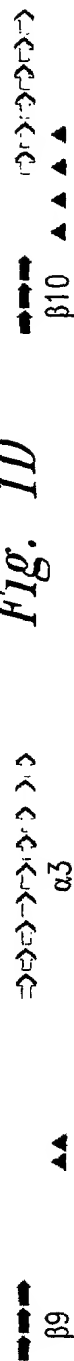


FIG. 1E

	280	290	300	310	320	330	340
Hum_PTP1B	LADTCLLLMDKR	KDPSSVDI	KKVLLLEMRKFRMG	LIQTADQLRFSYLA	LVIEGAKFIMGD		
Hum_TCPTP	LVDTCCLVLMKEG	DD	INI	KQVLLNMRKYRMG	LIQTPDQLRFSYMAI	IEGAKCIKGDSS	
Hum_PTP_xi_D1	VLDLMLQQIQHE	GT	VNI	FGFLKHIRSQRNY	LVQTEEQYVFIHDTL	VEAAILSKETEV	
Hum_PTP_zela_D1	VLDLMLQQIQHE	GT	VNI	FGFLKHIRSQRNY	LVQTEEQYVFIHDTL	VEAAILSKETEV	
Hum_PTP_gamma_D	VLDLMLQQIKDK	ST	VNV	LGFLKHIRTQRNY	LVQTEEQYIFIHDALE	AILGKETEV	
Dros_PTP99A_D1	VLDAMLKQIQK	NI	VNV	FGFLRHIRARQNF	LVQTEEQYIFLHDALE	VEAIASETNL	
Hum_LCA_D1	VLDAMLERMKHE	KT	VDI	YGHVTCMRSQRNY	MVQTEEQYVFIHEAL	LEAATCGHTEV	
Hum_PTP_mu_D1	VIDIMLDMAERE	GV	VDI	YNCVRELRSRRVN	MVQTEEQYVFIHDAI	LEACLCGDTSV	
Hum_PTP_alpha_D1	VIDAMLDMMHTE	RK	VDV	YGFVSRIARQRCQ	MVQTEEQYVFIYQAL	LEHYLYGDTL	
Hum_PTP_opsilon_D	VIDAMLMAMHAE	QK	VDV	YGFVSRIARQRCQ	MVQTEEQYVFIYQAL	LEHYLYGDTL	
Mouso_CD45_D1	VIDAMLEGLAE	GK	VDV	YGYVVKLRRQRCL	MVQTEAQYILIHQAL	VEYNQFGETEV	
Hum_SH.PTP2	VIDILIDIIREK	GL	VDV	PKTIQMVRSQRSG	MVQTEAQYRFIYMAV	QHYIETLQRR	
Hum_SH.PTP1	VIDMLMENISTK	GL	VDI	QKTIQMVRAQRSG	MVQTEAQYKFIYVAI	AQFIETTKKL	
Hum_PTP_bola	ALDRILQQLDSK	DS	VDI	YGAVDHLRLHRVH	MVQTECQYVYLHQ	CVDRDLRARKLRS	
Dros_PTP10D	TLDRILQQINTS	DY	VDI	FGIVYAMRKERVW	MVQTEQYICIHQCL	LAVLEGKENIVGP	
Hum_SAP.1	ALDVLLRQLQSE	GL	LGP	FSFVRKMRRESRPL	MVQTEAQYVFLHQ	CICGSSNSQPRPQPR	
Ral_PTP_STEP	ATSICCCQLRRE	GV	VDI	LKTTCCQLRQDRGG	MIQTECQYQFVHHAM	SLY	
Dros_PTP69A_D1	ALDSLIIQQLLEE	DS	VSI	YNTVCDLHQHNF	LVQSLKQYIFLYRAL	LDGTGFGNTDI	
Hum_MEG2	SLDICALQLEEL	GT	LNV	FQTVSRMRTQRAF	SIQTEPQYVFCYKA	ILEFA	
Hum_PTP.PEST	AIDYTNLILKAG	KIPEEFNV	FNLIQEMRTQRHS	AVQTEQYELVHRAI	AQLEFEKQLQLY		
Hum_PTPH1	TMETAMCLTERN	LP	IYP	LDIVRKMRDQRAM	MVQTESSQYKFCVCE	AILRVY	
Dici_PTP1	TAVIMMKKLDHYFK	QLDYNSRIDFNL	FSIVLKLREQRPG	MVQTEQYKFCYKTL	LDLDEIYHRLNC		
Fiss_yeast_pyp1	VLDITLRFPESKLSG	FNPVSADSSDVFL	VDHIRKQRMK	MVQTEQYKFCYKTL	LDLDEIYHRLNC		
Fiss_yeast_pyp2	AVDQILOVPKNILPK	TNLEDSKDFI	NCVNSLRSORMK	MVQTEQYKFCYKTL	LDLDEIYHRLNC		
Hum_PTP_xi_D2	VLDLMLQQIQHE	GT	VNI	FGFLKHIRSQRNY	LVQTEEQYVFIHDTL	VEAAILSKETEV	
Hum_LCA_D2	TLSTVLERMYE	GV	VDM	FQTVKTLRTQRP	MVQTEQYQLCYRAA	LEYL	
Hum_PTP_alpha_D2	ALSTVLERVKAE	GI	LDV	FQTVKSLRLQRP	MVQTEQYEFCKVQ	VEYI	
Hum_PTP_opsilon_D2	ALSNILERVKAE	GL	LDV	FQAVKSLRLQRP	MVQTEQYEFCKVQ	VQDFI	
Hum_PTP_mu_D2	AISIVCEMLRHQ	RT	VDV	FHAVKTLRNNKPN	MVDLLDQYKFCYEA	VEALEYLSG	
Mouse_CD45_D2	ALFNLLSAETE	DV	VDV	FQVVKSLRKARPG	VVCSYEQYQFLYDI	IASIYPAQNGQV	
Dros_PTP69A_D2	AMCIVLQHLRLE	KC	VDI	CATRKLRSGRTG	LINSYAQYEFHLRAI	INY	
Hum_PTP_zeia_D2	ALTTLMHQLEKE	NS	VDV	YQVAKMINLMRPG	VFADIEQYQFLYK	VILSLVSTRQEN	
Hum_PTP_gamma_D2	ALTTLSQOLENE	NA	VDV	FQVAKMINLMRPG	VFTDIEQYQFIYK	AMLSLVSTKENG	
Dros_PTP99A_D2	AISSLAIEMEYC	ST	ANV	YQYAKLYHNKRP	PG VFTSSEDIRVI	YN ILSELPGNLNLKR	
Yarsinia_PTP	GAMCMNDSRNSQ		LSV	EDMVSOMRVORNG	MVOKDEOLDVLIK	LAE	
PTP1Bseq.no.	230	240	250	260	270	280	

Fig. 1E

PTP1B66

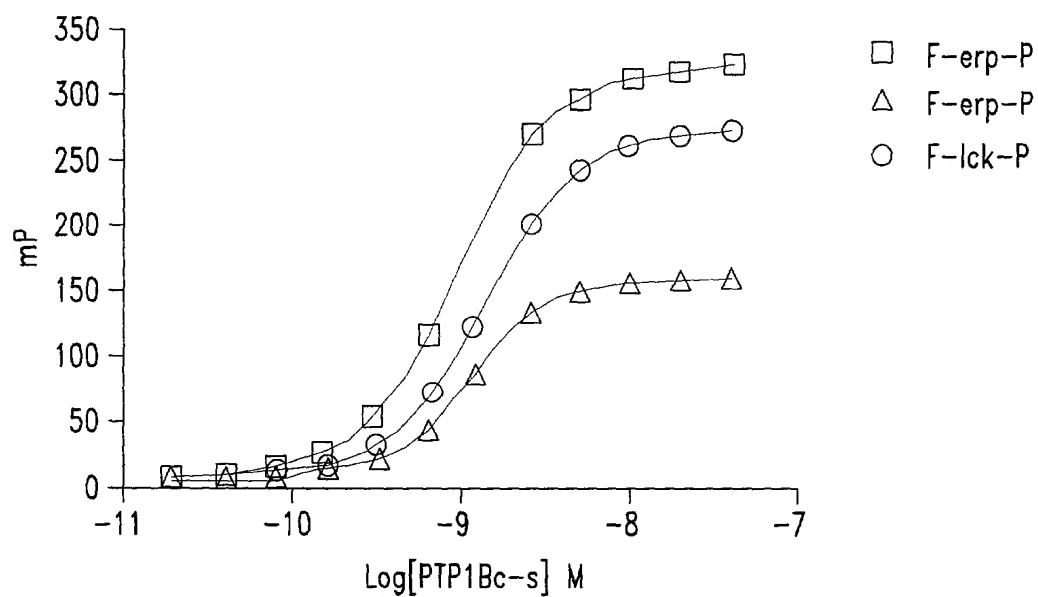


Fig. 2

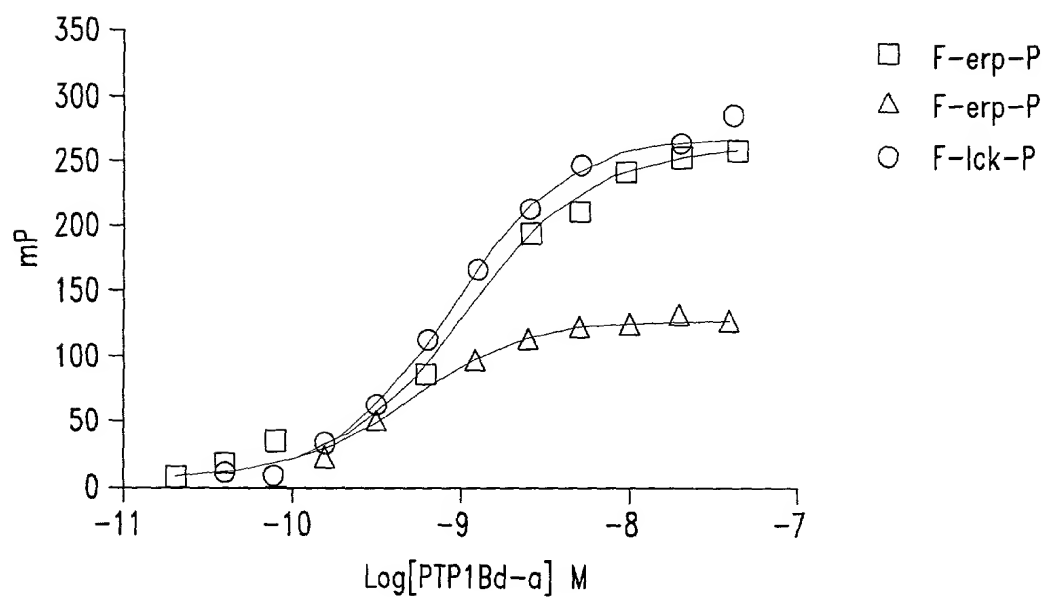


Fig. 3

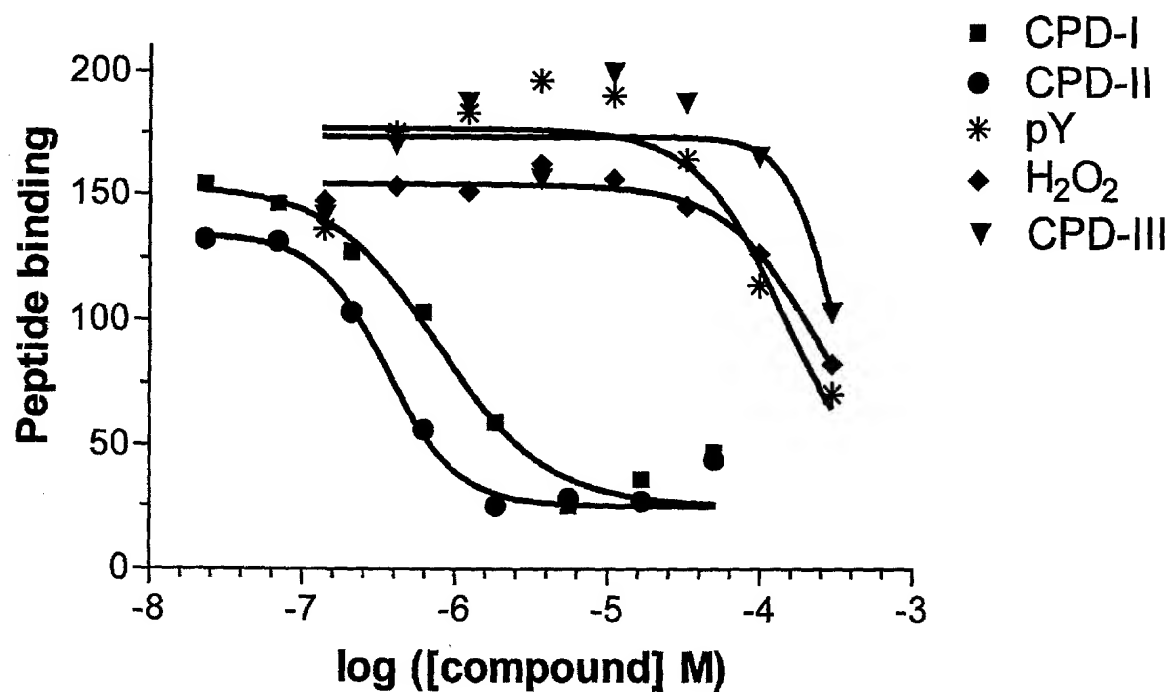


Fig. 4A

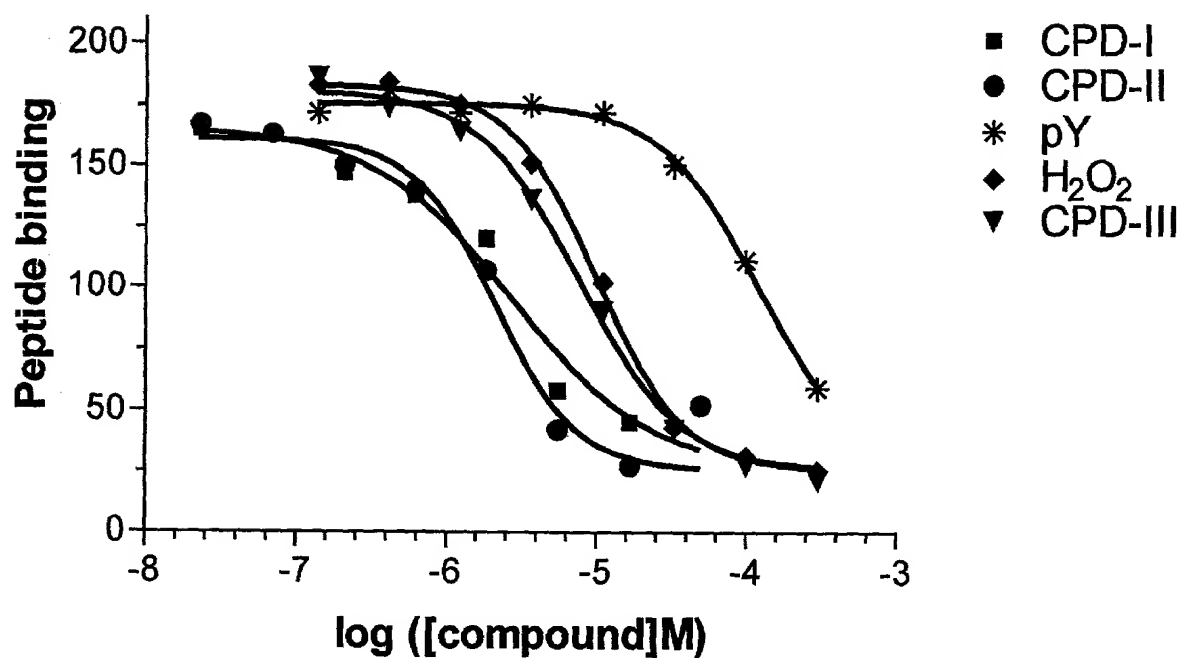


Fig. 4B

Binding of P-ERP: ERP mixture with G104

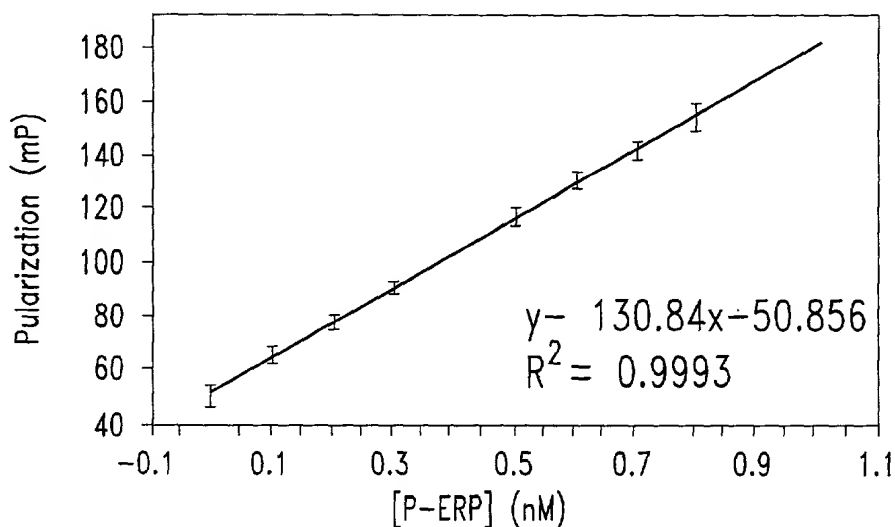


Fig. 5

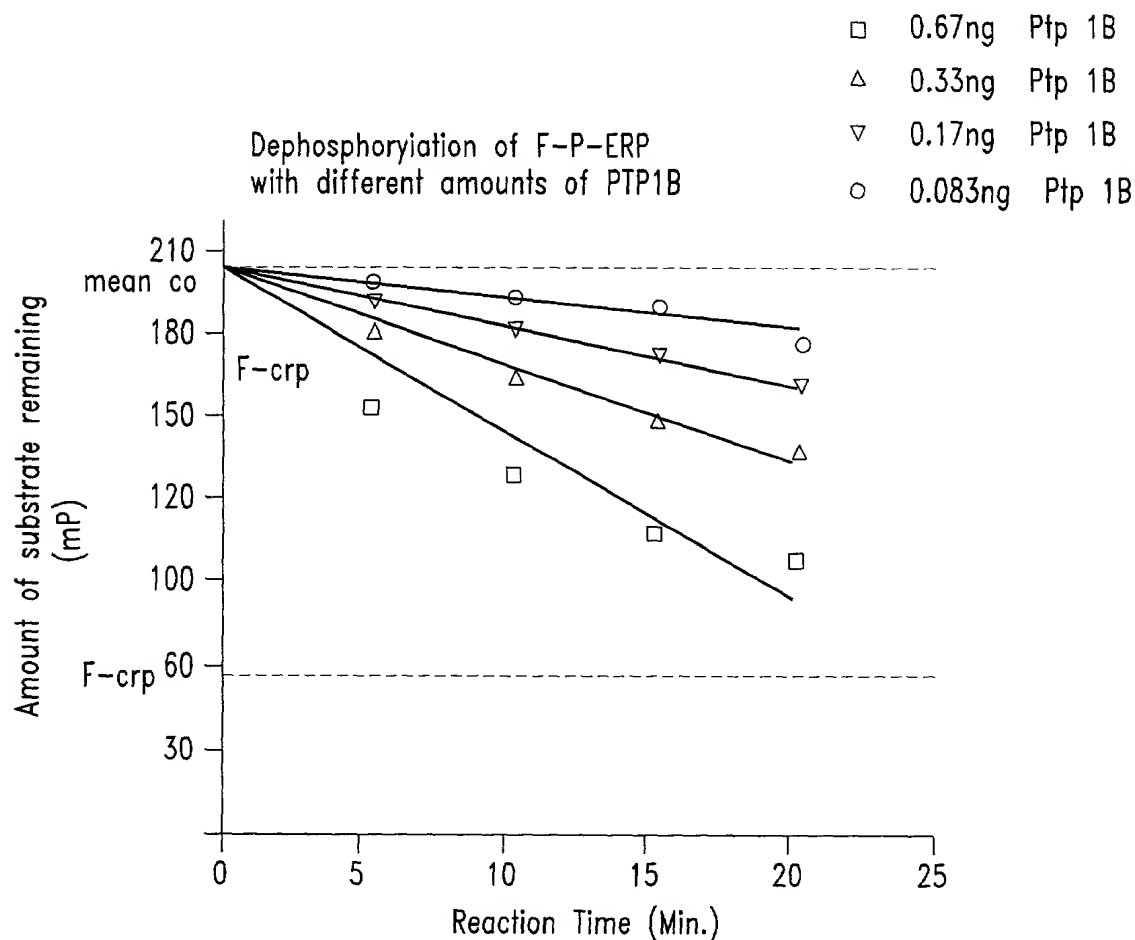


Fig. 6

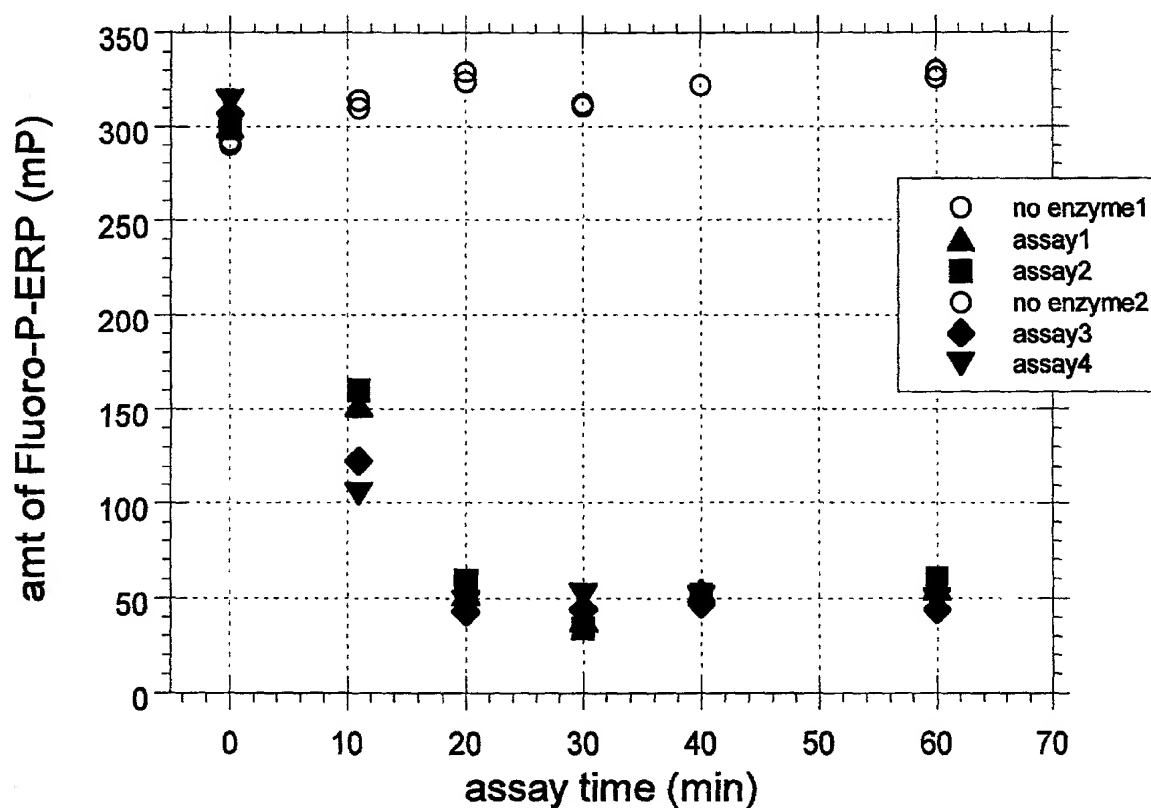


Fig. 7A

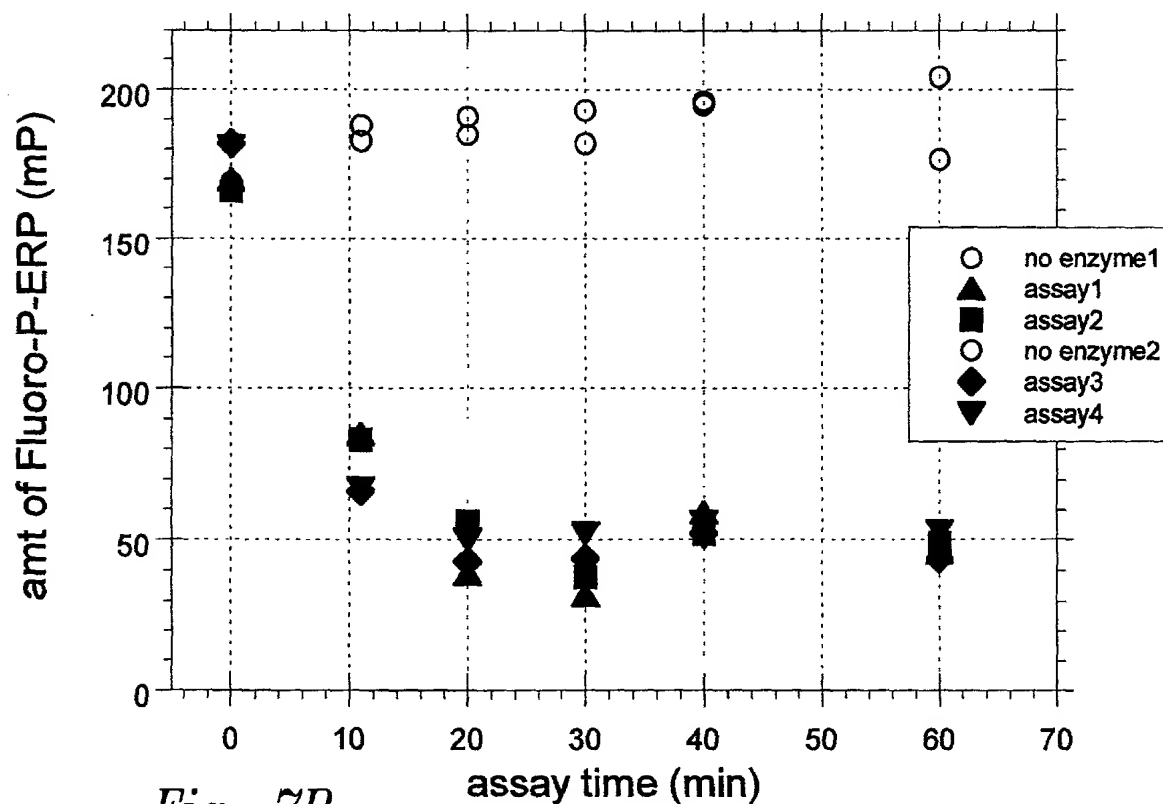


Fig. 7B

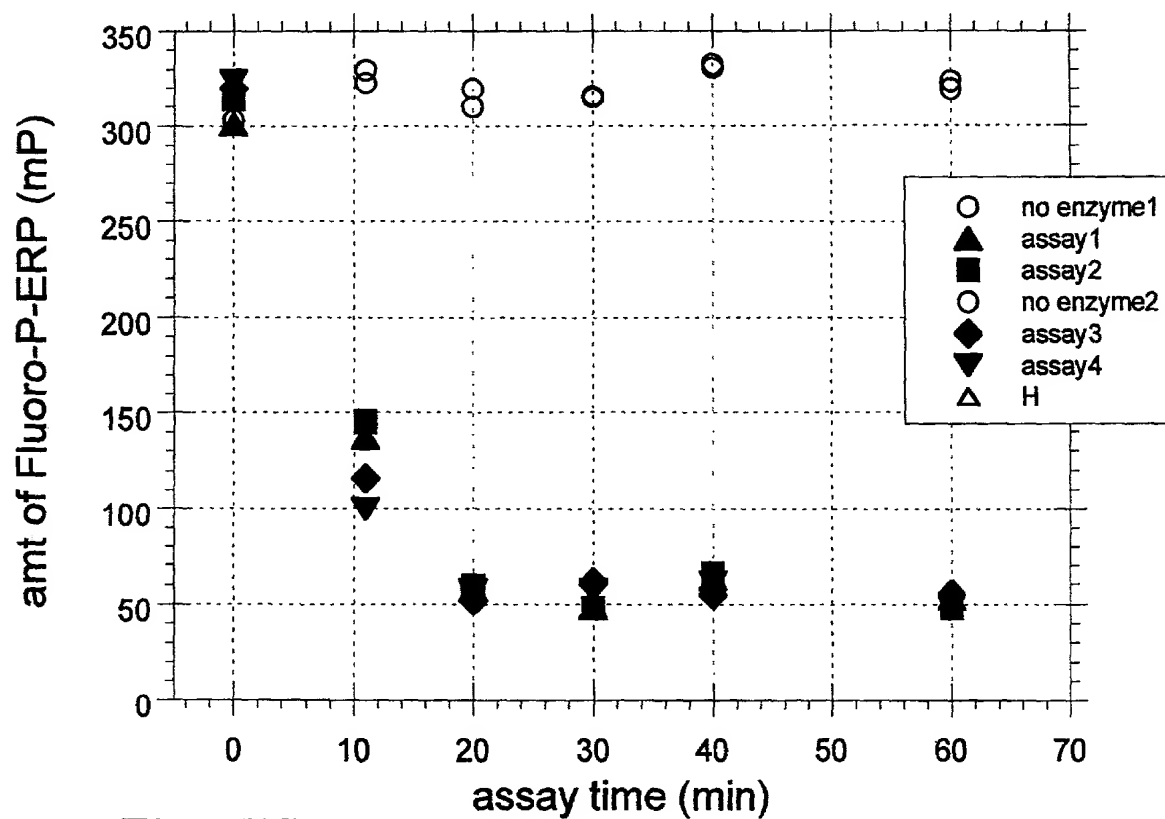


Fig. 7C

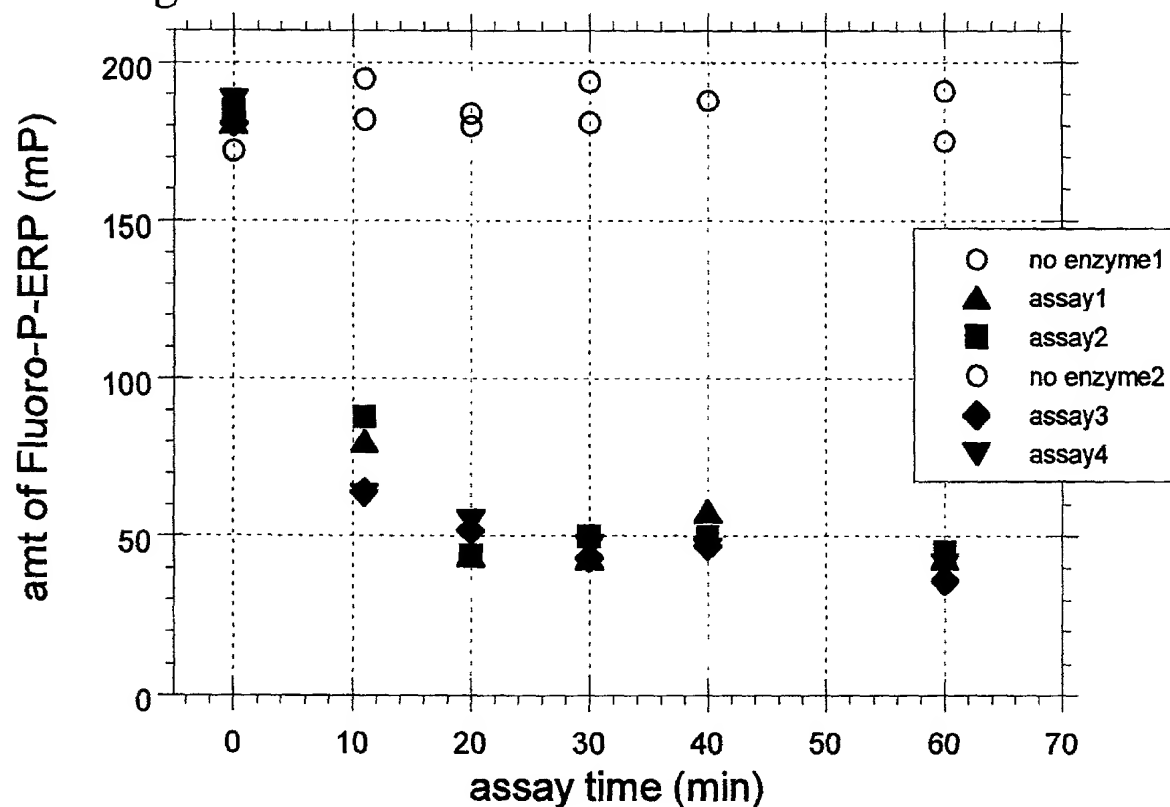


Fig. 7D

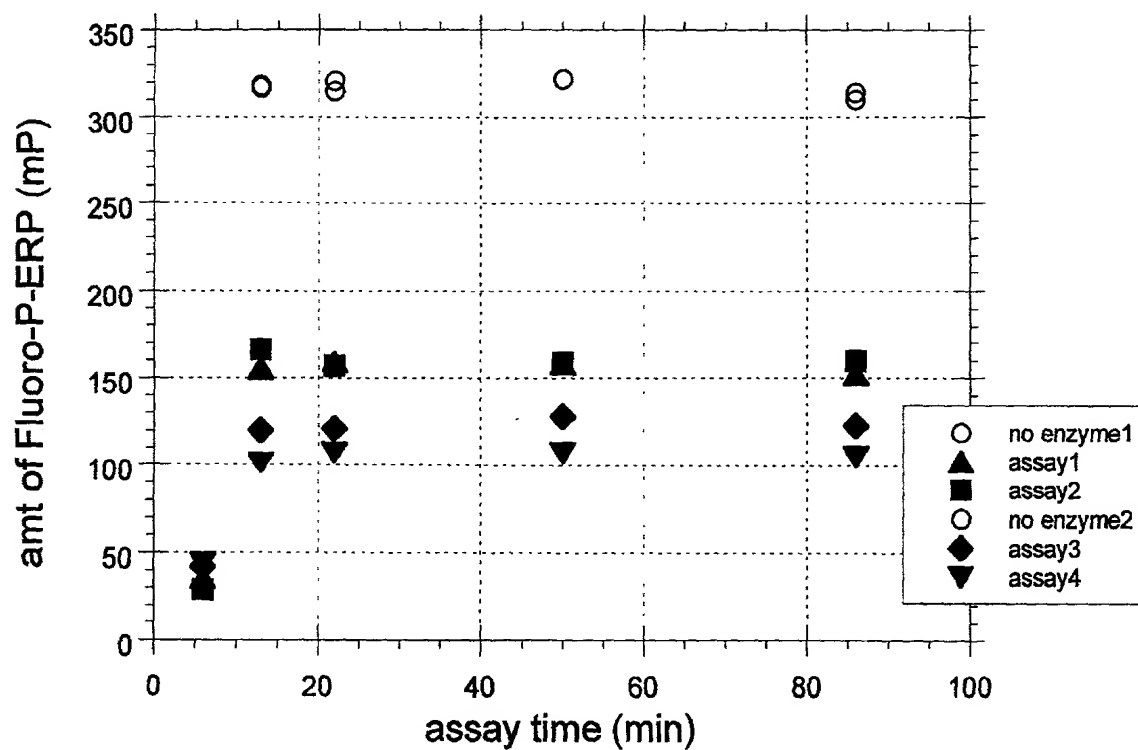


Fig. 8A

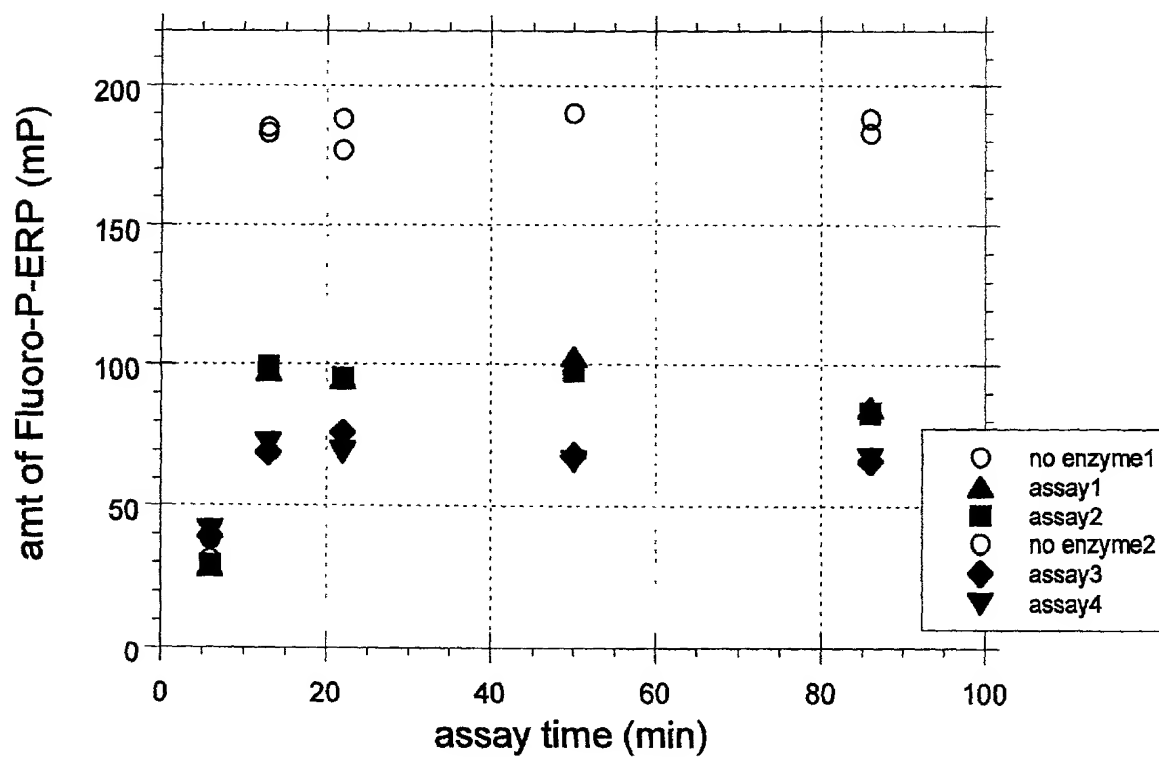


Fig. 8B

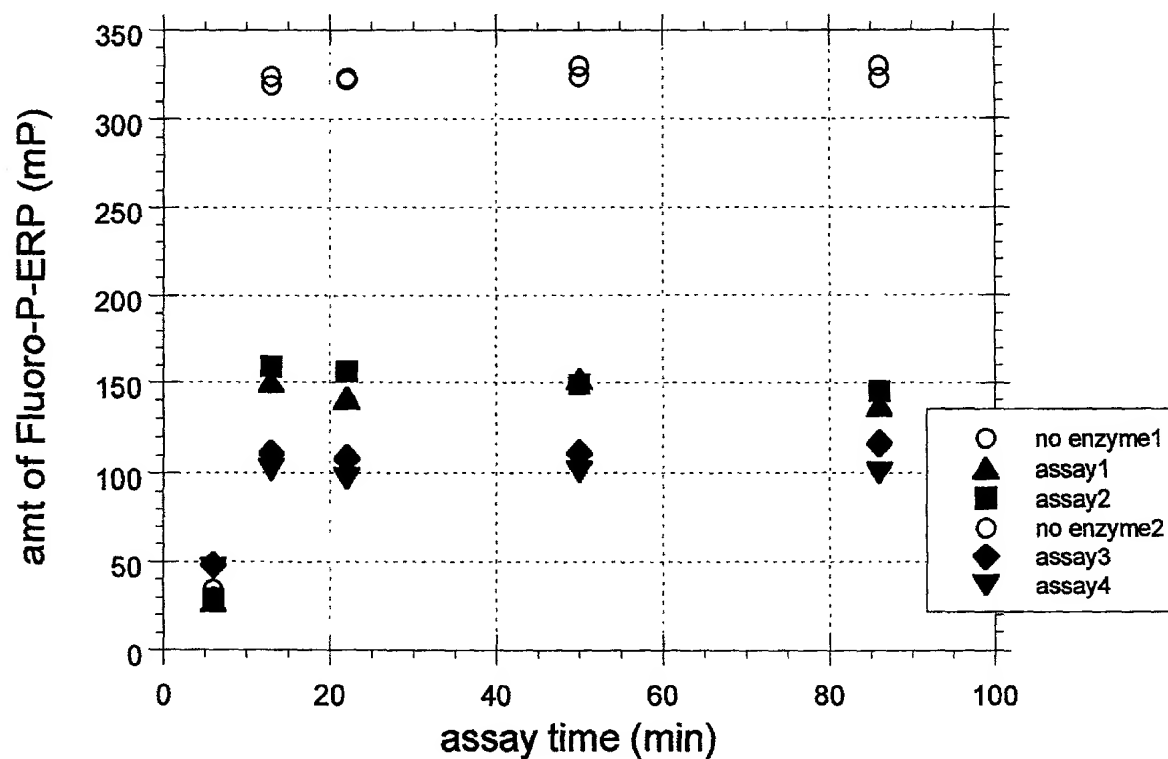


Fig. 8C

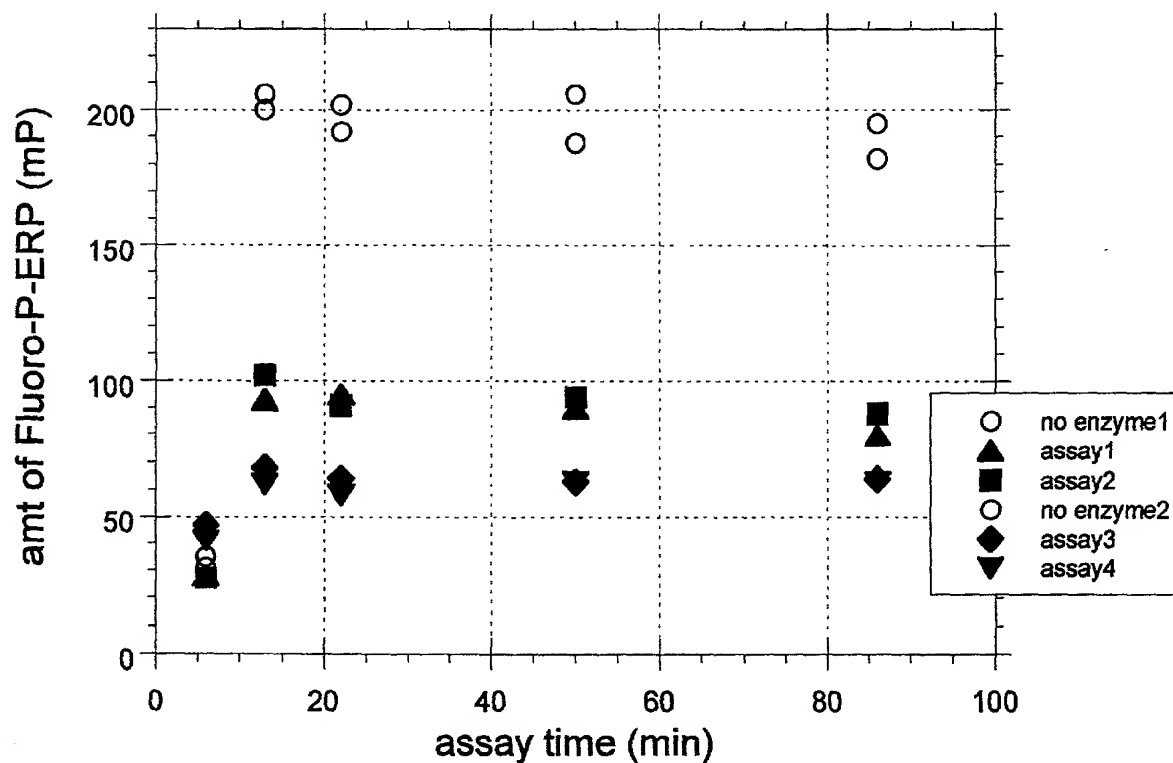


Fig. 8D

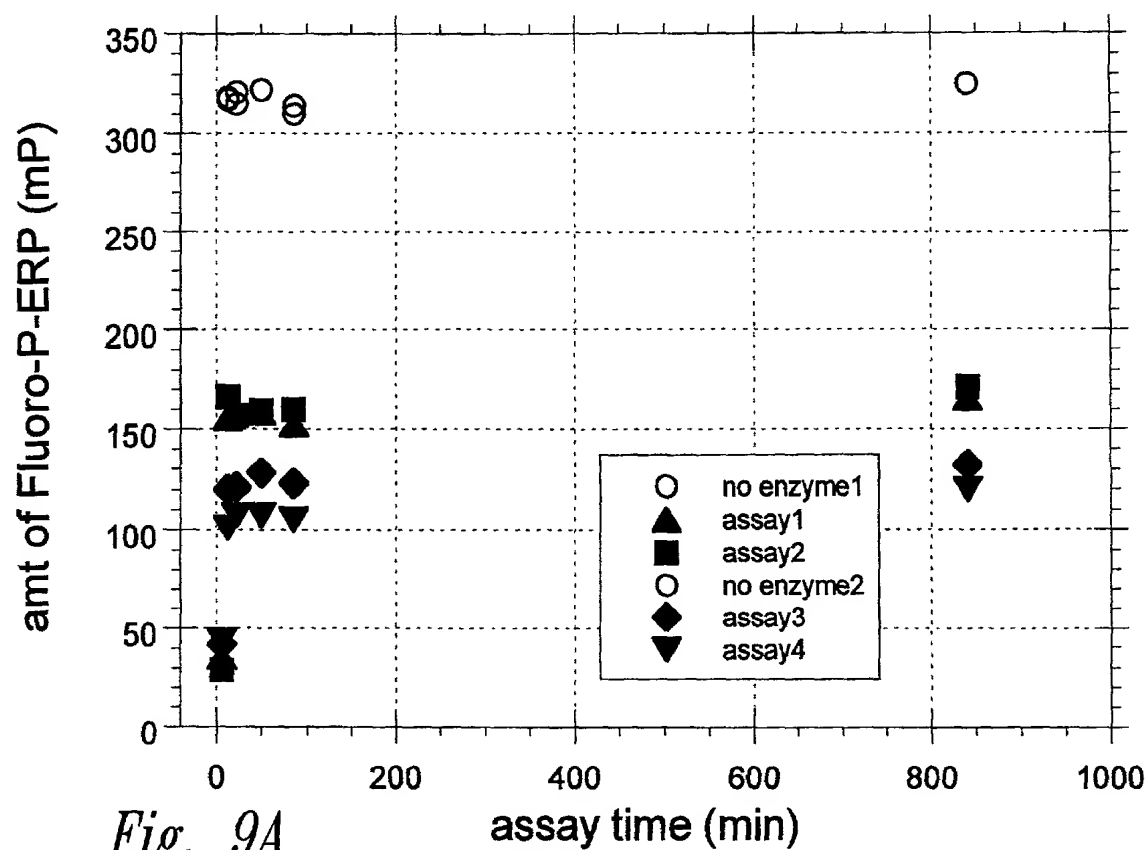


Fig. 9A

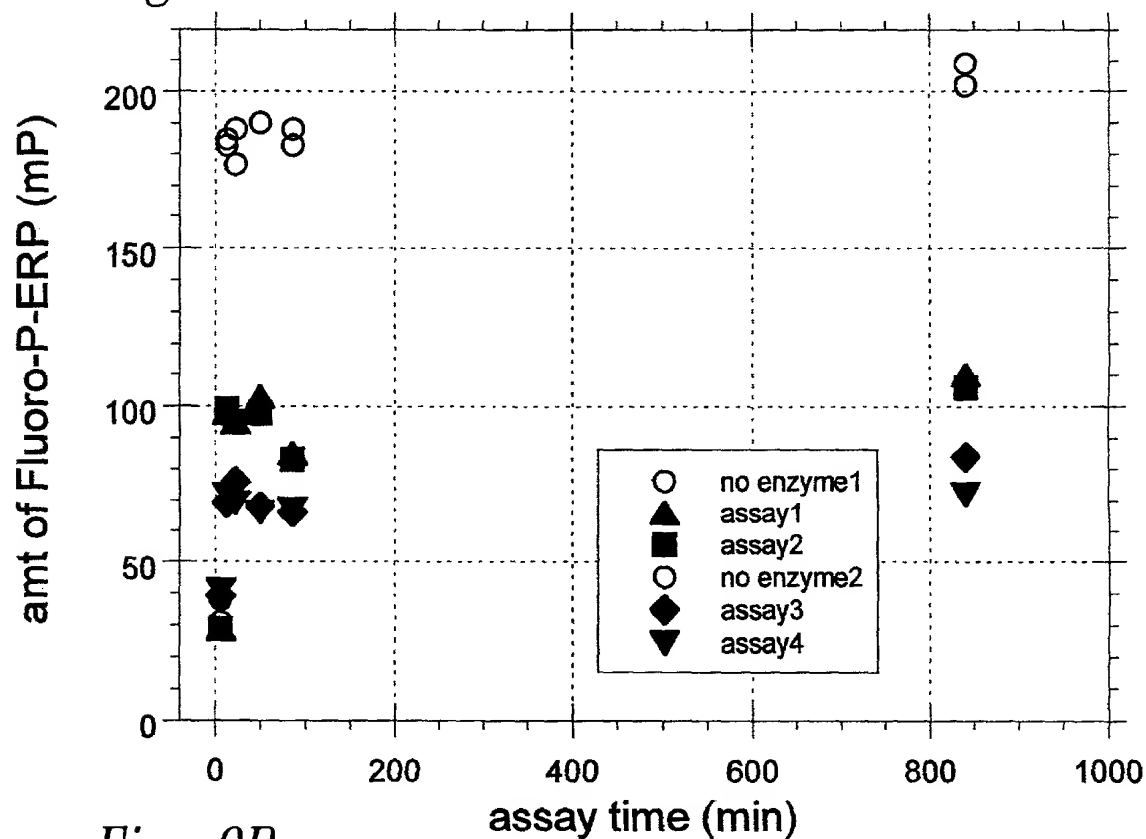
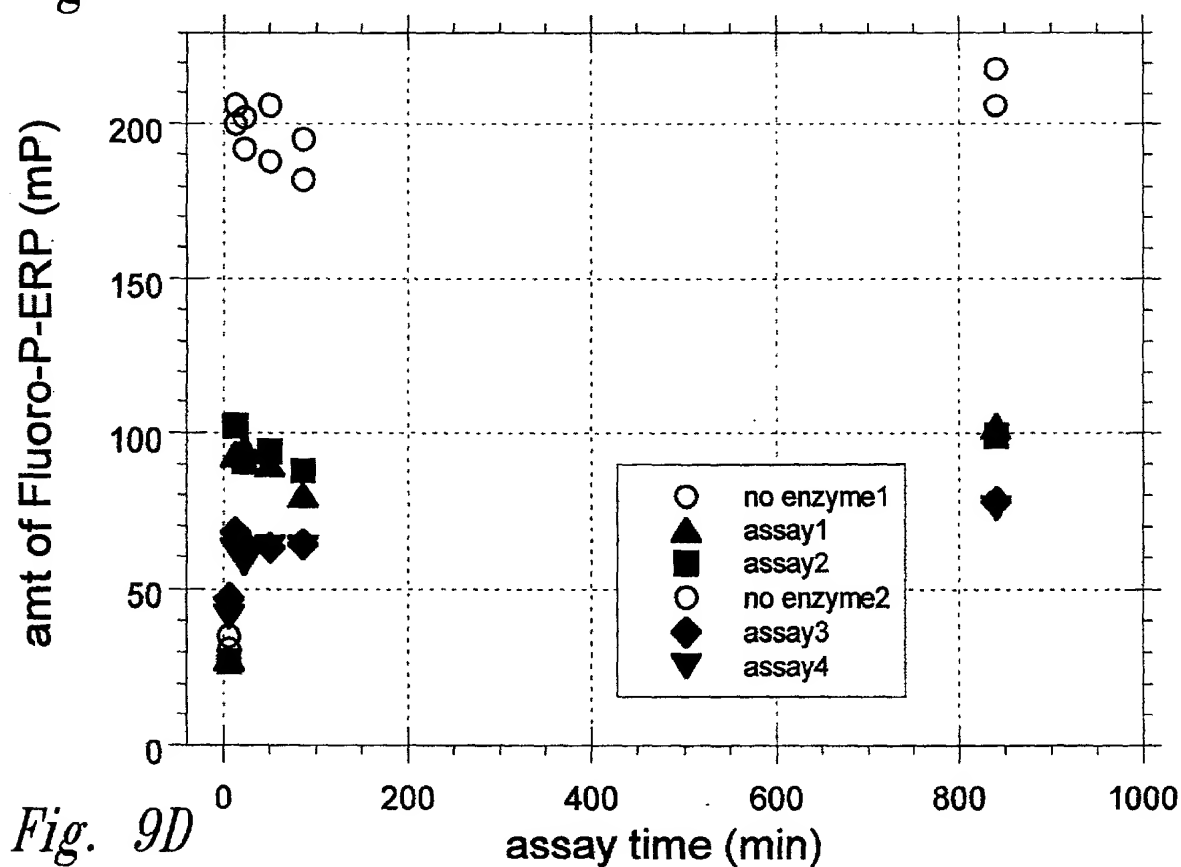
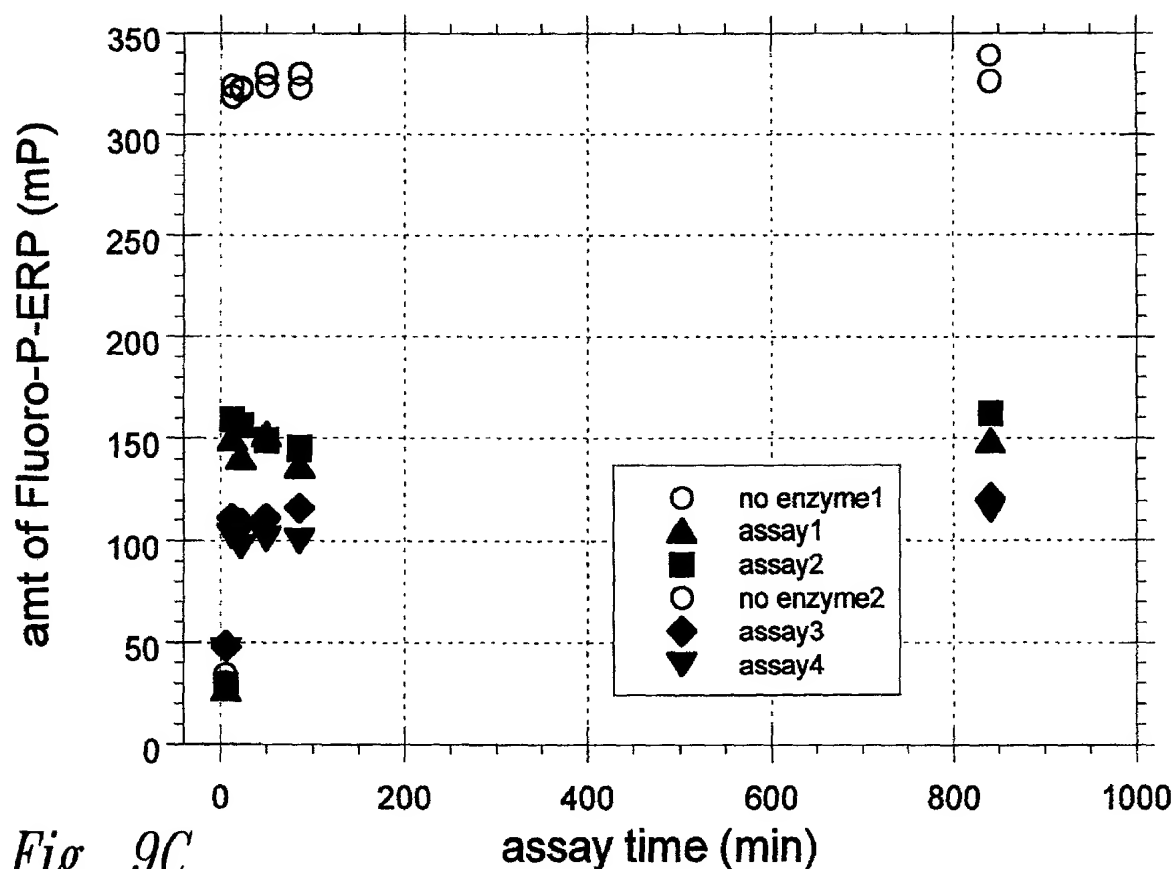


Fig. 9B



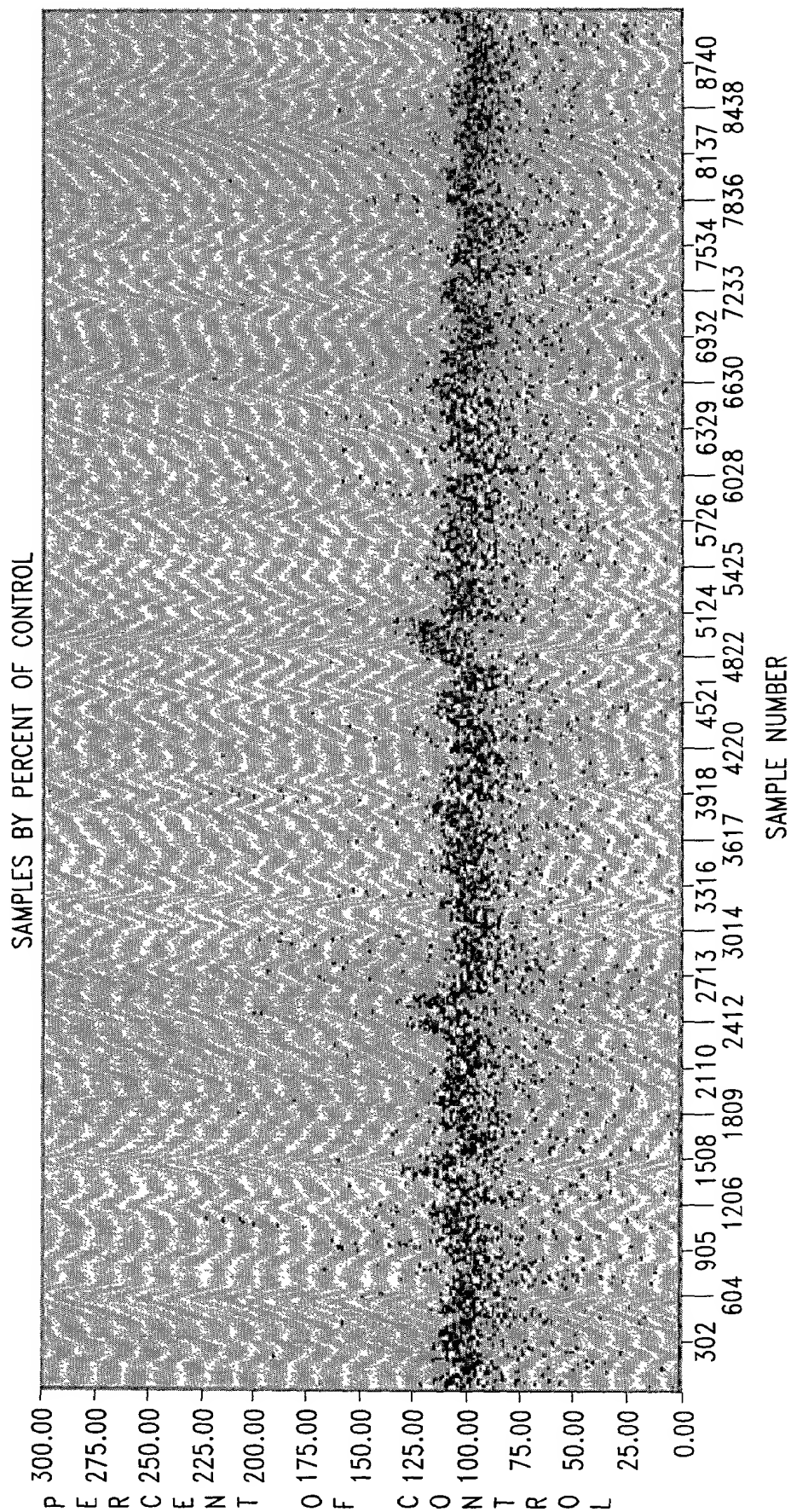


Fig. 10A

105090 9298860

SAMPLES BY PERCENT OF CONTROL

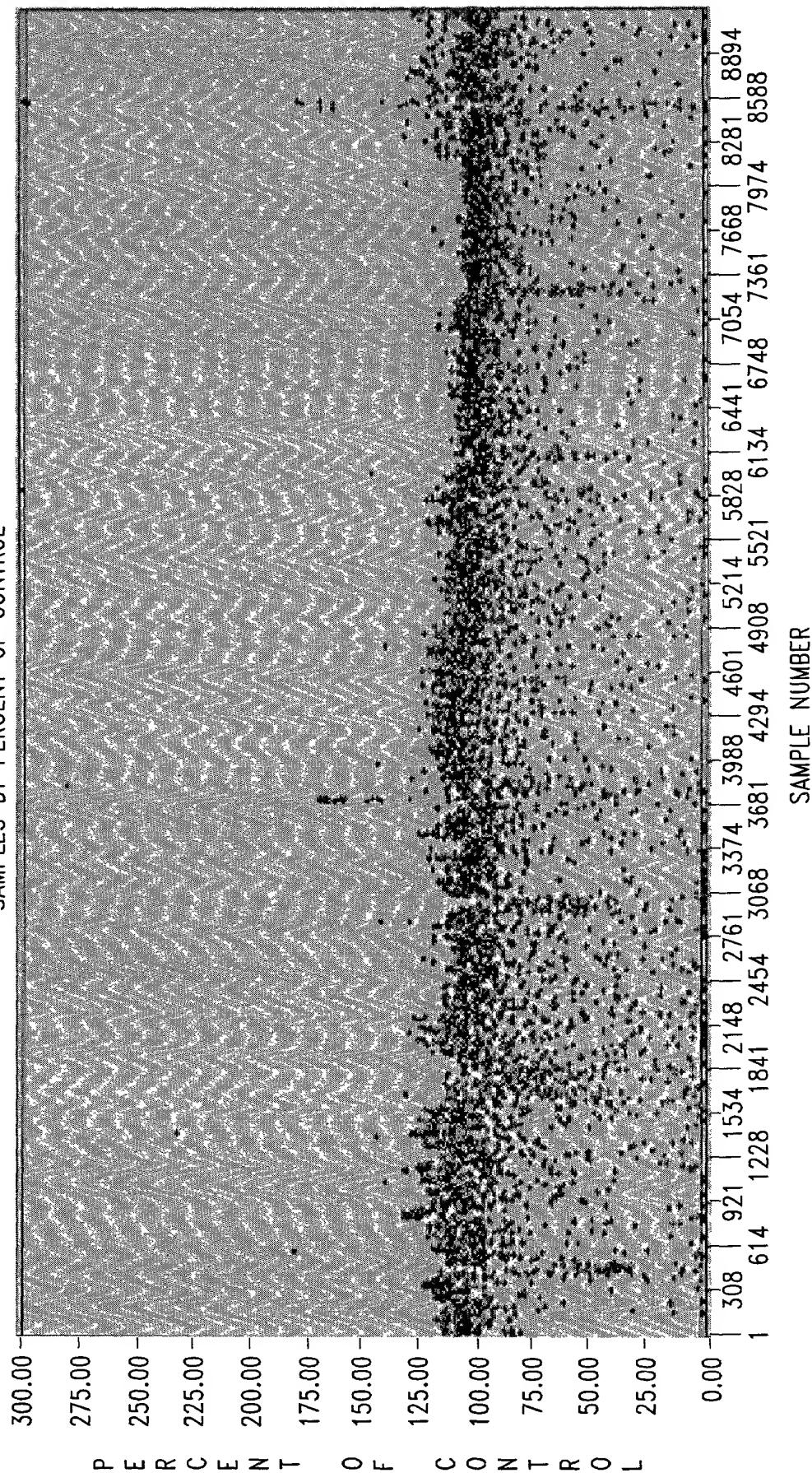


Fig. 10B